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PCT10

RAW SEQUENCE LISTING

DATE: 12/11/2002

PATENT APPLICATION: US/10/009,500A

TIME: 09:28:55

Input Set : N:\Crf4\11182002\J009500.raw

Output Set: N:\CRF4\12112002\J009500A.raw

1 <110> APPLICANT: KORDOWICZ, MARIA
 2 GUESSOW, DETLET
 3 HOFMANN, UWE
 4 PACUSZKA, TADEUSZ
 5 GARDAS, ANDRZEJ
 6 <120> TITLE OF INVENTION: HYALURONIDASE FROM THE HIRUDINARIA MANILLENSIS,
 7 ISOLATION, PURIFICATION AND RECOMBINANT METHOD OF
 8 PRODUCTION
 9 <130> FILE REFERENCE: MERCK 2332
 10 <140> CURRENT APPLICATION NUMBER: US/10/009,500A
 11 <141> CURRENT FILING DATE: 2002-04-08
 12 <160> NUMBER OF SEQ ID NOS: 20
 13 <170> SOFTWARE: PatentIn Ver. 2.1
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 488
 17 <212> TYPE: PRT
 18 <213> ORGANISM: Hirudinaria manillensis
 19 <400> SEQUENCE: 1
 20 Lys Glu Ile Ala Val Thr Ile Asp Asp Lys Asn Val Ile Ala Ser Val
 21 1 5 10 15
 22 Ser Glu Ser Phe His Gly Val Ala Phe Asp Ala Ser Leu Phe Ser Pro
 23 20 25 30
 24 Lys Gly Leu Trp Ser Phe Val Asp Ile Thr Ser Pro Lys Leu Phe Lys
 25 35 40 45
 26 Leu Leu Glu Gly Leu Ser Pro Gly Tyr Phe Arg Val Gly Gly Thr Phe
 27 50 55 60
 28 Ala Asn Trp Leu Phe Phe Asp Leu Asp Glu Asn Asn Lys Trp Lys Asp
 29 65 70 75 80
 30 Tyr Trp Ala Phe Lys Asp Lys Thr Pro Glu Thr Ala Thr Ile Thr Arg
 31 85 90 95
 32 Arg Trp Leu Phe Arg Lys Gln Asn Asn Leu Lys Lys Glu Thr Glu Asp
 33 100 105 110
 34 Asp Leu Val Lys Leu Thr Lys Gly Ser Lys Met Arg Leu Leu Phe Asp
 35 115 120 125
 36 Leu Asn Ala Glu Val Arg Thr Gly Tyr Glu Ile Gly Lys Lys Met Thr
 37 130 135 140
 38 Ser Thr Trp Asp Ser Ser Glu Ala Glu Lys Leu Phe Lys Tyr Cys Val
 39 145 150 155 160
 40 Ser Lys Gly Tyr Gly Asp Asn Ile Asp Trp Glu Leu Gly Asn Glu Pro
 41 165 170 175
 42 Asp His Thr Ser Ala His Asn Leu Thr Glu Lys Gln Val Gly Glu Asp
 43 180 185 190
 44 Phe Lys Ala Leu His Lys Val Leu Glu Lys Tyr Pro Thr Leu Asn Lys

mp 4-5
Does Not Comply
Corrected Diskette Needed

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Input Set : N:\Cr4\11182002\J009500.raw

Output Set: N:\CRF4\12112002\J009500A.raw

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45          195          200          205
46      Gly Ser Leu Val Gly Pro Asp Val Gly Trp Met Gly Val Ser Tyr Val
47          210          215          220
48      Lys Gly Leu Ala Asp Gly Ala Gly Asp Leu Val Thr Ala Phe Thr Leu
49      225          230          235          240
50      His Gln Tyr Tyr Phe Asp Gly Asn Thr Ser Asp Val Ser Thr Tyr Leu
51          245          250          255
52      Asp Ala Thr Tyr Phe Lys Lys Leu Gln Gln Leu Phe Asp Lys Val Lys
53          260          265          270
54      Asp Val Leu Lys Asn Ser Gln His Lys Asp Lys Pro Leu Trp Leu Gly
55          275          280          285
56      Glu Thr Ser Ser Gly Tyr Asn Ser Gly Thr Lys Asp Val Ser Asp Arg
57          290          295          300
58      Tyr Val Ser Gly Phe Leu Thr Leu Asp Lys Leu Gly Leu Ser Ala Ala
59      305          310          315          320
60      Asn Asn Val Lys Val Val Ile Arg Gln Thr Ile Tyr Asn Gly Tyr Tyr
61          325          330          335
62      Gly Leu Leu Asp Lys Asn Thr Leu Glu Pro Asn Pro Asp Tyr Trp Leu
63          340          345          350
64      Met His Val His Asn Ser Leu Val Gly Asn Thr Val Phe Lys Val Asp
65          355          360          365
66      Val Ser Asp Pro Thr Asn Lys Ala Arg Val Tyr Ala Gln Cys Thr Lys
67          370          375          380
68      Thr Asn Ser Lys His Thr Gln Ser Arg Tyr Tyr Lys Gly Ser Leu Thr
69      385          390          395          400
70      Ile Phe Ala Leu Asn Val Gly Asp Glu Asp Val Thr Leu Lys Ile Asp
71          405          410          415
72      Gln Tyr Gly Gly Lys Lys Ile Tyr Ser Tyr Ile Leu Thr Pro Glu Gly
73          420          425          430
74      Gly Gln Leu Thr Ser Gln Lys Val Leu Leu Asn Gly Lys Glu Leu Lys
75          435          440          445
76      Leu Val Ser Asp Gln Leu Pro Glu Leu Asn Ala Asn Glu Ser Lys Thr
77          450          455          460
78      Ser Phe Thr Leu Ser Pro Lys Thr Phe Gly Phe Phe Val Val Ser Asp
79      465          470          475          480
80      Ala Asn Val Glu Ala Cys Lys Lys
81          485

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83 <210> SEQ ID NO: 2

84 <211> LENGTH: 1464

85 <212> TYPE: DNA

86 <213> ORGANISM: Hirudinaria manillensis

87 <220> FEATURE:

88 <221> NAME/KEY: CDS

89 <222> LOCATION: (1)..(1464)

90 <400> SEQUENCE: 2

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91      aaa gag att gcc gtg aca att gac gat aag aat gtg att gca tct gcc      48
92      Lys Glu Ile Ala Val Thr Ile Asp Asp Lys Asn Val Ile Ala Ser Ala
93          1          5          10          15
94      agt ggg tct ttc ctt gga gtt gcc ttt gat gcg tct cta ttt tcg ccc      96

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RAW SEQUENCE LISTING

DATE: 12/11/2002

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TIME: 09:28:55

Input Set : N:\Crf4\11182002\J009500.raw

Output Set: N:\CRF4\12112002\J009500A.raw

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144          275          280          285
145    gaa aca agt tct gga tac aac agc ggc aca gaa gat gta tcc gat cga    912
146    Glu Thr Ser Ser Gly Tyr Asn Ser Gly Thr Glu Asp Val Ser Asp Arg
147          290          295          300
148    tat gtt tca gga ttt cta aca tta gac aag ttg ggt ctc agt gca gcc    960
149    Tyr Val Ser Gly Phe Leu Thr Leu Asp Lys Leu Gly Leu Ser Ala Ala
150    305          310          315          320
151    aac aat gta aag gtt gtt ata aga cag aca ata tac aat gga tat tat    1008
152    Asn Asn Val Lys Val Val Ile Arg Gln Thr Ile Tyr Asn Gly Tyr Tyr
153          325          330          335
154    ggt ctc ctt gac aaa aac act tta gag ccg aat ccg gat tac tgg tta    1056
155    Gly Leu Leu Asp Lys Asn Thr Leu Glu Pro Asn Pro Asp Tyr Trp Leu
156          340          345          350
157    atg cat gtt cat aat tct ttg gtc gga aat aca gtt ttt aaa gtt gac    1104
158    Met His Val His Asn Ser Leu Val Gly Asn Thr Val Phe Lys Val Asp
159          355          360          365
160    gtt agt gat cca act aat aaa gca aga gtt tac gcg caa tgt acc aaa    1152
161    Val Ser Asp Pro Thr Asn Lys Ala Arg Val Tyr Ala Gln Cys Thr Lys
162    370          375          380
163    aca aat agc aaa cat act caa agc aga tat tac aag ggc tct ttg aca    1200
164    Thr Asn Ser Lys His Thr Gln Ser Arg Tyr Tyr Lys Gly Ser Leu Thr
165    385          390          395          400
166    atc ttt gca ctt aat gtt gga gat gga gat gta acg tta aag atc ggt    1248
167    Ile Phe Ala Leu Asn Val Gly Asp Gly Asp Val Thr Leu Lys Ile Gly
168          405          410          415
169    caa tac agc ggt aaa aaa att tat tca tac att ctg aca cct gaa gga    1296
170    Gln Tyr Ser Gly Lys Lys Ile Tyr Ser Tyr Ile Leu Thr Pro Glu Gly
171          420          425          430
172    gga caa ctt aca tca cag aaa gtt ctc ttg aat gga aag gaa ttg aac    1344
173    Gly Gln Leu Thr Ser Gln Lys Val Leu Leu Asn Gly Lys Glu Leu Asn
174          435          440          445
175    tta gtg tct gat cag tta cca gaa cta aat gca gat gaa tcc aaa aca    1392
176    Leu Val Ser Asp Gln Leu Pro Glu Leu Asn Ala Asp Glu Ser Lys Thr
177    450          455          460
178    tct ttc acc tta tcc cca aag aca ttt ggt ttt ttt gtt gtt tcc gat    1440
179    Ser Phe Thr Leu Ser Pro Lys Thr Phe Gly Phe Phe Val Val Ser Asp
180    465          470          475          480
181    gct aat gtt gaa gca tgy aar aar    1464
182    Ala Asn Val Glu Ala Cys Lys Lys
183          485

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185 <210> SEQ ID NO: 3
186 <211> LENGTH: 488
187 <212> TYPE: PRT
188 <213> ORGANISM: Hirudinaria manillensis
189 <220> FEATURE:
190 <221> NAME/KEY: variation
191 <222> LOCATION: (223)
192 <223> OTHER INFORMATION: (May be Asn)
193 <400> SEQUENCE: 3

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Please Correct any
similar error
in subsequent sequences

(See p-5)
"Tyr" is at location 223. Tyr can
only represent itself nothing
else. Use Xaa and explain in
L2207 - L2237 section.

RAW SEQUENCE LISTING

DATE: 12/11/2002

PATENT APPLICATION: US/10/009,500A

TIME: 09:28:55

Input Set : N:\CrF4\11182002\J009500.raw

Output Set: N:\CRF4\12112002\J009500A.raw

95	Ser Gly Ser Phe Leu Gly Val Ala Phe Asp Ala Ser Leu Phe Ser Pro	
96		20 25 30
97	aag ggt ctt tgg agc ttt gtt gat att acc tct cca aaa ttg ttc aaa	144
98	Lys Gly Leu Trp Ser Phe Val Asp Ile Thr Ser Pro Lys Leu Phe Lys	
99		35 40 45
100	ttg ctg gaa gga ctt tct cct gga tac ttc agg gtt ggc gga acg ttt	192
101	Leu Leu Glu Gly Leu Ser Pro Gly Tyr Phe Arg Val Gly Gly Thr Phe	
102		50 55 60
103	gcc aat tgg ctg ttt ttt gac ttg gac gaa aat aat aag tgg aag gat	240
104	Ala Asn Trp Leu Phe Phe Asp Leu Asp Glu Asn Asn Lys Trp Lys Asp	
105		65 70 75 80
106	tat tgg gct ttt aaa gac aaa acc ccc gaa act gcg aca ata aca agg	288
107	Tyr Trp Ala Phe Lys Asp Lys Thr Pro Glu Thr Ala Thr Ile Thr Arg	
108		85 90 95
109	aga tgg ctg ttc aga aaa caa aat aat ctg aaa aag gag act ttt gac	336
110	Arg Trp Leu Phe Arg Lys Gln Asn Asn Leu Lys Lys Glu Thr Phe Asp	
111		100 105 110
112	aat tta gtg aaa cta aca aag gga agc aag atg aga ttg tta ttc gat	384
113	Asn Leu Val Lys Leu Thr Lys Gly Ser Lys Met Arg Leu Leu Phe Asp	
114		115 120 125
115	ttg aat gcc gaa gtg agg act ggt tat gaa att gga aag aag atg aca	432
116	Leu Asn Ala Glu Val Arg Thr Gly Tyr Glu Ile Gly Lys Lys Met Thr	
117		130 135 140
118	tcc act tgg gat tca tcg gag gct gaa aag tta ttt aaa tat tgt gtg	480
119	Ser Thr Trp Asp Ser Ser Glu Ala Glu Lys Leu Phe Lys Tyr Cys Val	
120		145 150 155 160
121	tca aaa ggt tac gga gac aat atc gat tgg gaa ctt gga aat gaa ccg	528
122	Ser Lys Gly Tyr Gly Asp Asn Ile Asp Trp Glu Leu Gly Asn Glu Pro	
123		165 170 175
124	gac cac acc tca gct cac aat tta act gaa aag cag gtt gga gaa gat	576
125	Asp His Thr Ser Ala His Asn Leu Thr Glu Lys Gln Val Gly Glu Asp	
126		180 185 190
127	ttt aaa gca ctg cat aaa gtt cta gag aaa tat cca act ctt aac aag	624
128	Phe Lys Ala Leu His Lys Val Leu Glu Lys Tyr Pro Thr Leu Asn Lys	
129		195 200 205
130	gga tcg ctc gtt ggt cca gat gta ggg tgg atg ggc gtc agt wac gtc	672
131	Gly Ser Leu Val Gly Pro Asp Val Gly Trp Met Gly Val Ser Tyr Val	
132		210 215 220
133	aag gga ttg gca gac gag gcr ggt gac cat gta ack gct ttt aca ctc	720
134	Lys Gly Leu Ala Asp Glu Ala Gly Asp His Val Thr Ala Phe Thr Leu	
135		225 230 235 240
136	cac caa tat tat ttc gat gga aac acy tct gat gta tca ata tat ctt	768
137	His Gln Tyr Tyr Phe Asp Gly Asn Thr Ser Asp Val Ser Ile Tyr Leu	
138		245 250 255
139	gat gcc aca tac ttt aag aag ctg caa caa cta ttt gat aaa gtg aaa	816
140	Asp Ala Thr Tyr Phe Lys Lys Leu Gln Gln Leu Phe Asp Lys Val Lys	
141		260 265 270
142	gat gtt ttg aaa gat tct cca cat aaa gac gaa cca tta tgg ctt gga	864
143	Asp Val Leu Lys Asp Ser Pro His Lys Asp Glu Pro Leu Trp Leu Gly	

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194   Lys Glu Ile Ala Val Thr Ile Asp Asp Lys Asn Val Ile Ala Ser Ala
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196   Ser Gly Ser Phe Leu Gly Val Ala Phe Asp Ala Ser Leu Phe Ser Pro
197               20               25               30
198   Lys Gly Leu Trp Ser Phe Val Asp Ile Thr Ser Pro Lys Leu Phe Lys
199               35               40               45
200   Leu Leu Glu Gly Leu Ser Pro Gly Tyr Phe Arg Val Gly Gly Thr Phe
201       50               55               60
202   Ala Asn Trp Leu Phe Phe Asp Leu Asp Glu Asn Asn Lys Trp Lys Asp
203       65               70               75               80
204   Tyr Trp Ala Phe Lys Asp Lys Thr Pro Glu Thr Ala Thr Ile Thr Arg
205               85               90               95
206   Arg Trp Leu Phe Arg Lys Gln Asn Asn Leu Lys Lys Glu Thr Phe Asp
207               100              105              110
208   Asn Leu Val Lys Leu Thr Lys Gly Ser Lys Met Arg Leu Leu Phe Asp
209               115              120              125
210   Leu Asn Ala Glu Val Arg Thr Gly Tyr Glu Ile Gly Lys Lys Met Thr
211       130              135              140
212   Ser Thr Trp Asp Ser Ser Glu Ala Glu Lys Leu Phe Lys Tyr Cys Val
213       145              150              155              160
214   Ser Lys Gly Tyr Gly Asp Asn Ile Asp Trp Glu Leu Gly Asn Glu Pro
215               165              170              175
216   Asp His Thr Ser Ala His Asn Leu Thr Glu Lys Gln Val Gly Glu Asp
217               180              185              190
218   Phe Lys Ala Leu His Lys Val Leu Glu Lys Tyr Pro Thr Leu Asn Lys
219               195              200              205
220   Gly Ser Leu Val Gly Pro Asp Val Gly Trp Met Gly Val Ser Tyr Val
221       210              215              220
222   Lys Gly Leu Ala Asp Glu Ala Gly Asp His Val Thr Ala Phe Thr Leu
223       225              230              235              240
224   His Gln Tyr Tyr Phe Asp Gly Asn Thr Ser Asp Val Ser Ile Tyr Leu
225               245              250              255
226   Asp Ala Thr Tyr Phe Lys Lys Leu Gln Gln Leu Phe Asp Lys Val Lys
227               260              265              270
228   Asp Val Leu Lys Asp Ser Pro His Lys Asp Glu Pro Leu Trp Leu Gly
229               275              280              285
230   Glu Thr Ser Ser Gly Tyr Asn Ser Gly Thr Glu Asp Val Ser Asp Arg
231       290              295              300
232   Tyr Val Ser Gly Phe Leu Thr Leu Asp Lys Leu Gly Leu Ser Ala Ala
233       305              310              315              320
234   Asn Asn Val Lys Val Val Ile Arg Gln Thr Ile Tyr Asn Gly Tyr Tyr
235               325              330              335
236   Gly Leu Leu Asp Lys Asn Thr Leu Glu Pro Asn Pro Asp Tyr Trp Leu
237               340              345              350
238   Met His Val His Asn Ser Leu Val Gly Asn Thr Val Phe Lys Val Asp
239               355              360              365
240   Val Ser Asp Pro Thr Asn Lys Ala Arg Val Tyr Ala Gln Cys Thr Lys
241       370              375              380
242   Thr Asn Ser Lys His Thr Gln Ser Arg Tyr Tyr Lys Gly Ser Leu Thr

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VERIFICATION SUMMARY

DATE: 12/11/2002

PATENT APPLICATION: US/10/009,500A

TIME: 09:28:56

Input Set : N:\Crf4\11182002\J009500.raw

Output Set: N:\CRF4\12112002\J009500A.raw